

-1-

SEQUENCE LISTING

<110> Vertino, Paula M.

<120> TMS1 Compositions and Methods of Use

<130> E0355/7003/ERG/MAT

<150> US 60/159,975

<151> 1999-10-18

<160> 27

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2821

<212> DNA

<213> Homo Sapiens

<400> 1

aagcttttga	atacaacatg	ctgcaggcat	cacagcctca	ttcattcctt	cactcagcaa	60
atctttactc	agcacctaata	gtgttccaga	tacatttttt	tttttcagat	ggaatctagc	120
tctgtcaccc	aggctggagt	gcagtgggtgc	aatcttggct	cactgtagcc	tctgcctccg	180
aggttcaagc	gattctcatg	cctcagccgc	cctagtagct	aggattacag	gcgccctcca	240
ccacacacag	ctatttccag	gtacattctt	gacgctagga	attcagcaaa	gaataagaca	300
gttaaggtct	ccgatgctca	taggcctcac	attttagaga	gggatgaatg	tccaataagc	360
atataaacat	ataatatgtc	agggtcgtat	gactacaagg	aacagtgatt	gttacaaccc	420
agatgagagg	gaaaaataaa	ggattccaaa	tatccccctt	gggaagtaga	gtcaggattc	480
aaacaaagaa	ctgtatggct	tcaagttcat	ggctctttaa	ctcctggagg	ctgtctctct	540
ttcttttttc	ttttttttaa	tcagtgttgg	gatcaaattc	tggctcccct	aggaagcatc	600
tggcaagggt	tccggagcca	tccgggttggc	catgttatgc	tggaaatatt	ataagcaccc	660
gagggttatc	cccattgtcg	agaaaatgaa	actgaagctc	agagagattt	gcactctctg	720
ccctttttgta	caactcattt	ttccccagta	tgttggaattg	agggagcttc	acgcttctag	780
ctgtcatgat	tccaagattc	tacgacatgt	gggagaggat	cctaagggtt	ggggaaccgc	840
ggaggtttcg	gggttctaga	aatccgaggt	tctaagccta	ggtgctccaa	taaaccagct	900
gagagccagc	ccagggtttcc	ggtctgtacc	cgctgggtgca	agcccagaga	caagcaggcg	960
ccacccatga	gcccctctgc	ggccccctcc	cgggtcccac	ctcgcaggcc	agctggaggg	1020
cgcgatcctg	gcgtcccccg	acggcctggg	gccccaatcc	agaggcctgg	gtgggagggg	1080
accaaggggtg	tagtaaggaa	gcgccttttg	ctggagggga	acggaccggg	gcggggagtc	1140
gggagaccag	agtgggagga	aggcggggag	tccagggttc	gccccggagc	cgacttcctc	1200
ctgggtcggcg	gctgcagcgg	ggtgagcggc	ggcagcggcc	ggggatcctg	gagccatggg	1260
gcgcgcgcgc	gacgccatcc	tggatgcgct	ggagaacctg	accgccgagg	agctcaagaa	1320
gttcaagctg	aagctgctgt	cgggtccgct	gcgcgagggc	tacgggcgca	tcccgcgggg	1380
cgcgctgctg	tccatggacg	ccttggaacct	caccgacaag	ctggctagct	tctacctgga	1440
gacctacggc	gccgagctca	ccgctaacct	gctgcgcgac	atgggcctgc	aggagatggc	1500
cgggcagctg	caggcggcca	cgcaccaggg	tgagccgccc	ccgttcccct	ccaccccgtc	1560
tttccccctc	acccacacca	gcgcttacct	cgcgggctct	tccgctttct	gttcctccta	1620
cccctaaaca	aagctgctct	accggaaagg	aggctcccca	cgcttggcct	accgaccaac	1680
gggacccccg	ccccacggcg	ggaagggaag	ggaaggggat	cacttggccc	atatccttcc	1740
aggctctgga	gccgcgccag	ctgggatcca	ggccccctct	cagtcggcag	ccaagccagg	1800
tgaggcctcc	acacccagcc	cggccccacc	gcactcctgc	acagcctgca	tctgtgctcc	1860
cgcaaccagg	gcagggcagg	gcagggcagg	cacggcttgg	caaccctgcg	cacccccacc	1920
accaacccac	accctgcggg	ggaagggaga	caatattacc	ctcatcccac	tgcattgtgg	1980
gtcctgggtg	ccgccccctg	gagccctgcc	cctaggcttg	cagaggaatt	cctgaagaac	2040
tcaagttcag	cagggacagg	ccccacaccc	tggctgctgg	ctcatgttct	cctcccaccc	2100
ccaggcctgc	actttataga	ccagcaccgg	gctgcgctta	tcgcgagggt	cacaaacggt	2160
gagtggtctg	tggatgctct	gtacgggaag	gtcctgacgg	atgagcagta	ccaggcagtg	2220

cgggccgagc ccaccaaccc aagcaagatg cggaagctct tcagtttcac accagcctgg 2280
aactggacct gcaaggactt gctcctccag gccctaaggg agtcccagtc ctacctgggtg 2340
gaggacctgg agcggagctg aggctccttc ccagcaacac tccggtcagc ccctggcaat 2400
cccaccaaata catcctgaat ctgatctttt tatacacaaat atacgaaaag ccagcttgaa 2460
cttgtgtgtt ttcctgcttc tagcctgctg gcatgtgcag agctcagcta tgcttcagag 2520
gccaccacagc ctccagctcc atgtccctag ggtctctggc accccaaatg cttcccccat 2580
ccttcctgggt atcgccatgg aatatccctc ctcatcacc aggtgggtgct cctccagtgc 2640
tccctaaagg gtctaaccct accattatag ataacagcct gtgaccacag tccgaagggt 2700
aaaagaggca tgtaccaaag ggcgcaaact ggtgggcagc tctgtccaag ccatttagaa 2760
acacactagt cttcatagct cccctacctt ccacattttc cactggaaga aaaaatggca 2820
a 2821

<210> 2
<211> 770
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (75)...(662)

<400> 2

ccacgcgtcc gacttctctc tggtcggcgg ctgcagcggg gtgagcggcg gcagcggccg 60
gggatacctgg agcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg 110
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu
1 5 10
gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg 158
Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu
15 20 25
tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg 206
Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
30 35 40
ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac 254
Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
45 50 55 60
ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg 302
Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met
65 70 75
ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc 350
Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly
80 85 90
tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca gcc 398
Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala
95 100 105
aag cca ggc ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg 446
Lys Pro Gly Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala
110 115 120
agg gtc aca aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc 494
Arg Val Thr Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val
125 130 135 140
ctg acg gat gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca 542

Leu Thr Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro	
145 150 155	
agc aag atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc	590
Ser Lys Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr	
160 165 170	
tgc aag gac ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg	638
Cys Lys Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu	
175 180 185	
gtg gag gac ctg gag cgg agc tga ggctccttcc cagcaacact ccggtcagcc	692
Val Glu Asp Leu Glu Arg Ser *	
190 195	
cctggcaatc ccaccaaatc atcctgaatc tgatcttttt atacacaata tacgaaaagc	752
cagcttgaaa aaaaaaaaa	770

<210> 3
 <211> 195
 <212> PRT
 <213> Homo Sapiens

<400> 3																	
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr																	
1 5 10 15																	
Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu																	
20 25 30																	
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp																	
35 40 45																	
Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr																	
50 55 60																	
Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu																	
65 70 75 80																	
Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala																	
85 90 95																	
Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu																	
100 105 110																	
His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn																	
115 120 125																	
Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu																	
130 135 140																	
Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg																	
145 150 155 160																	
Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu																	
165 170 175																	
Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu																	
180 185 190																	
Glu Arg Ser																	
195																	

<210> 4
 <211> 626
 <212> DNA
 <213> Homo Sapiens

<400> 4																	
agcgcctttt gctggagggc aacggaccgg ggcggggagt cgggagacca gagtgggagg	60																
aaggcgggga gtccaggttc cgccccggag ccgacttcct cctggtcggc ggctgcagcg	120																
gggtgagcgg cggcagcggc cggggatcct ggagccatgg ggcgcgcgcg cgacgccatc	180																

ctggatgcgc	tggagaacct	gaccgccgag	gagctcaaga	agttcaagct	gaagctgctg	240
tcggtgccgc	tgcgcgaggg	ctacggggcg	atccccgcgg	gcgcgctgct	gtccatggac	300
gccttggacc	tcaccgacaa	gctggtcagc	ttctacctgg	agacctacgg	cgccgagctc	360
accgctaacg	tgctgcgcga	catgggcctg	caggagatgg	ccgggcagct	gcaggcgggc	420
acgcaccagg	gtgagccgcc	cccgttcccc	tcacccccgt	ctttcccctc	cacccacacc	480
agcgcttacc	ccgcggggctc	ttccgctttc	tggttcctcct	acccctaaac	aaagctgctc	540
taccggaaag	gaggctcccc	acgcttgccc	taccgaccaa	cgggaccccg	gccccacggc	600
gggaagggaa	gggaagggga	tcactt				626

<210> 5
 <211> 339
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> (67)...(339)

<400> 5																
ccgacttcct	cctggtcggc	ggctgcagcg	gggtgagcgg	cggcagcggc	cggggatcct										60	
ggagcc	atg	ggg	cgc	gcg	cgc	gac	gcc	atc	ctg	gat	gcg	ctg	gag	aac	108	
	Met	Gly	Arg	Ala	Arg	Asp	Ala	Ile	Leu	Asp	Ala	Leu	Glu	Asn		
	1					5						10				
ctg	acc	gcc	gag	gag	ctc	aag	aag	ttc	aag	ctg	aag	ctg	ctg	tcg	gtg	156
Leu	Thr	Ala	Glu	Glu	Leu	Lys	Lys	Phe	Lys	Leu	Lys	Leu	Leu	Ser	Val	
15					20					25				30		
ccg	ctg	cgc	gag	ggc	tac	ggg	cgc	atc	ccg	cgg	ggc	gcg	ctg	ctg	tcc	204
Pro	Leu	Arg	Glu	Gly	Tyr	Gly	Arg	Ile	Pro	Arg	Gly	Ala	Leu	Leu	Ser	
				35				40						45		
atg	gac	gcc	ttg	gac	ctc	acc	gac	aag	ctg	gtc	agc	ttc	tac	ctg	gag	252
Met	Asp	Ala	Leu	Asp	Leu	Thr	Asp	Lys	Leu	Val	Ser	Phe	Tyr	Leu	Glu	
			50					55					60			
acc	tac	ggc	gcc	gag	ctc	acc	gct	aac	gtg	ctg	cgc	gac	atg	ggc	ctg	300
Thr	Tyr	Gly	Ala	Glu	Leu	Thr	Ala	Asn	Val	Leu	Arg	Asp	Met	Gly	Leu	
		65					70					75				
cag	gag	atg	gcc	ggg	cag	ctg	cag	gcg	gcc	acg	cac	cag	g			340
Gln	Glu	Met	Ala	Gly	Gln	Leu	Gln	Ala	Ala	Thr	His	Gln				
	80					85					90					

<210> 6
 <211> 91
 <212> PRT
 <213> Homo Sapiens

<400> 6															
Met	Gly	Arg	Ala	Arg	Asp	Ala	Ile	Leu	Asp	Ala	Leu	Glu	Asn	Leu	Thr
1				5					10					15	
Ala	Glu	Glu	Leu	Lys	Lys	Phe	Lys	Leu	Lys	Leu	Leu	Ser	Val	Pro	Leu
			20					25					30		
Arg	Glu	Gly	Tyr	Gly	Arg	Ile	Pro	Arg	Gly	Ala	Leu	Leu	Ser	Met	Asp
		35				40						45			
Ala	Leu	Asp	Leu	Thr	Asp	Lys	Leu	Val	Ser	Phe	Tyr	Leu	Glu	Thr	Tyr
	50					55					60				
Gly	Ala	Glu	Leu	Thr	Ala	Asn	Val	Leu	Arg	Asp	Met	Gly	Leu	Gln	Glu

80

<220>
<221> CDS
<222> (3) ... (58)

47

57

57

57

57

47

95

143

191

gac ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg gtg gag 239
Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu
65 70 75

gac ctg gag cgg agc tga g gctccttccc agcaacactc cggtcagccc 288
Asp Leu Glu Arg Ser *
80

ctggcaatcc caccaaatac tcctgaatct gatcttttta tacacaatat acgaaaagcc 348
agcttgaa 356

<210> 10
<211> 84
<212> PRT
<213> Homo Sapiens

<400> 10
Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr
1 5 10 15
Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp
20 25 30
Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met
35 40 45
Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp
50 55 60
Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp
65 70 75 80
Leu Glu Arg Ser

<210> 11
<211> 18
<212> DNA
<213> Homo Sapiens

<400> 11
gcactttata gaccagca 18

<210> 12
<211> 18
<212> DNA
<213> Homo Sapiens

<400> 12
atttggtggg attgccag 18

<210> 13
<211> 17
<212> DNA
<213> Homo Sapiens

<400> 13
tgggcctgca ggagatg 17

<210> 14
<211> 22
<212> DNA
<213> Homo Sapiens

<400> 14

ccttcctggg catggagtcc tg 22

<210> 15
<211> 21
<212> DNA
<213> Homo Sapiens

<400> 15
ggagcaatga tcttgatcct c 21

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Primer

<400> 16
ggttgtagtg gggtagtgg t 21

<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Primer

<400> 17
caaaacatcc ataaacaaca acaca 25

<210> 18
<211> 19
<212> DNA
<213> Homo Sapiens

<400> 18
ttgtagcggg gtgagcggc 19

<210> 19
<211> 22
<212> DNA
<213> Homo Sapiens

<400> 19
aacgtccata aacaacaacg cg 22

<210> 20
<211> 803
<212> DNA
<213> Mus Musculus

<220>
<221> CDS
<222> (162)...(743)

<400> 20
gggaaagaac aggagctgta agaaaagagg gtgggggagt cccagcatgc ccatcggcct 60
aagcagctga cttcctggtc ttggcgggct ggcagcaggc aggctgagca ggcgagcagc 120

agcaagagta aaaggtgacc gcggtgccc accccagagc c atg ggg cgg gca cga	176
Met Gly Arg Ala Arg	
1 5	
gat gcc atc ctg gac gct ctt gaa aac ttg tca ggg gat gaa ctc aaa	224
Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Ser Gly Asp Glu Leu Lys	
10 15 20	
aag ttc aag atg aag ctg ctg aca gtg caa ctg cga gaa ggc tat ggg	272
Lys Phe Lys Met Lys Leu Leu Thr Val Gln Leu Arg Glu Gly Tyr Gly	
25 30 35	
cgc atc cca cgc ggg gcc ctg ctg cag atg gac gcc ata gat ctc act	320
Arg Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Ala Ile Asp Leu Thr	
40 45 50	
gac aaa ctt gtc agc tac tat ctg gag tcg tat ggc ttg gag ctc aca	368
Asp Lys Leu Val Ser Tyr Tyr Leu Glu Ser Tyr Gly Leu Glu Leu Thr	
55 60 65	
atg act gtg ctt aga gac atg ggc tta cag gag ctg gct gag cag ctg	416
Met Thr Val Leu Arg Asp Met Gly Leu Gln Glu Leu Ala Glu Gln Leu	
70 75 80 85	
caa acg act aaa gaa gag tct gga gct gtg gca gct gca gcc agt gtc	464
Gln Thr Thr Lys Glu Glu Ser Gly Ala Val Ala Ala Ala Ala Ser Val	
90 95 100	
cct gct cag agt aca gcc aga aca gga cac ttt gtg gac cag cac agg	512
Pro Ala Gln Ser Thr Ala Arg Thr Gly His Phe Val Asp Gln His Arg	
105 110 115	
caa gca ctc att gcc agg gtc aca gaa gtg gac gga gtg ctg gat gct	560
Gln Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Val Leu Asp Ala	
120 125 130	
ttg cat ggc agt gtg ctg act gaa gga cag tac cag gca gtt cgt gca	608
Leu His Gly Ser Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala	
135 140 145	
gag acc acc agc caa gac aag atg agg aag ctc ttc agc ttt gtt cca	656
Glu Thr Thr Ser Gln Asp Lys Met Arg Lys Leu Phe Ser Phe Val Pro	
150 155 160 165	
tcc tgg aac ctg acc tgc aag gac tcc ctc ctc cag gcc ttg aag gaa	704
Ser Trp Asn Leu Thr Cys Lys Asp Ser Leu Leu Gln Ala Leu Lys Glu	
170 175 180	
ata cat ccc tac ttg gtg atg gac ctg gag cag agc tga ggtatctttt	753
Ile His Pro Tyr Leu Val Met Asp Leu Glu Gln Ser *	
185 190	
ccagctacat tatctagctc ctgactttgt atacacaatt tttgaaaaaa	803

<210> 21
 <211> 193
 <212> PRT
 <213> Mus Musculus

<400> 21

Met	Gly	Arg	Ala	Arg	Asp	Ala	Ile	Leu	Asp	Ala	Leu	Glu	Asn	Leu	Ser
1				5					10					15	
Gly	Asp	Glu	Leu	Lys	Lys	Phe	Lys	Met	Lys	Leu	Leu	Thr	Val	Gln	Leu
			20					25						30	
Arg	Glu	Gly	Tyr	Gly	Arg	Ile	Pro	Arg	Gly	Ala	Leu	Leu	Gln	Met	Asp
		35				40						45			
Ala	Ile	Asp	Leu	Thr	Asp	Lys	Leu	Val	Ser	Tyr	Tyr	Leu	Glu	Ser	Tyr
	50					55					60				
Gly	Leu	Glu	Leu	Thr	Met	Thr	Val	Leu	Arg	Asp	Met	Gly	Leu	Gln	Glu
65					70					75					80
Leu	Ala	Glu	Gln	Leu	Gln	Thr	Thr	Lys	Glu	Glu	Ser	Gly	Ala	Val	Ala
			85						90					95	
Ala	Ala	Ala	Ser	Val	Pro	Ala	Gln	Ser	Thr	Ala	Arg	Thr	Gly	His	Phe
			100					105					110		
Val	Asp	Gln	His	Arg	Gln	Ala	Leu	Ile	Ala	Arg	Val	Thr	Glu	Val	Asp
		115					120					125			
Gly	Val	Leu	Asp	Ala	Leu	His	Gly	Ser	Val	Leu	Thr	Glu	Gly	Gln	Tyr
	130					135					140				
Gln	Ala	Val	Arg	Ala	Glu	Thr	Thr	Ser	Gln	Asp	Lys	Met	Arg	Lys	Leu
145					150					155					160
Phe	Ser	Phe	Val	Pro	Ser	Trp	Asn	Leu	Thr	Cys	Lys	Asp	Ser	Leu	Leu
			165					170						175	
Gln	Ala	Leu	Lys	Glu	Ile	His	Pro	Tyr	Leu	Val	Met	Asp	Leu	Glu	Gln
			180					185					190		

Ser

<210> 22
 <211> 605
 <212> DNA
 <213> Rattus Norvegicus
 <220>
 <221> CDS
 <222> (2)...(518)

<400> 22

t	ttc	aag	ata	aag	ctg	ctg	aca	gcg	cca	gtg	cgg	gaa	ggc	tat	ggg	cgc	49
	Phe	Lys	Ile	Lys	Leu	Leu	Thr	Ala	Pro	Val	Arg	Glu	Gly	Tyr	Gly	Arg	
1				5						10					15		
atc	cca	cgg	ggg	gcc	ctg	ctg	cag	atg	gac	ccc	ata	gac	ctc	act	gat		97
Ile	Pro	Arg	Gly	Ala	Leu	Leu	Gln	Met	Asp	Pro	Ile	Asp	Leu	Thr	Asp		
			20					25					30				
aaa	ctc	gtc	agy	tac	tat	ctg	gag	ggg	tat	ggc	ttg	gag	ctc	aca	atg		145
Lys	Leu	Val	Xaa	Tyr	Tyr	Leu	Glu	Gly	Tyr	Gly	Leu	Glu	Leu	Thr	Met		
		35					40					45					
act	gtg	ctt	aga	gac	atg	ggc	ata	cag	gag	ctg	gct	gag	cag	ctg	caa		193
Thr	Val	Leu	Arg	Asp	Met	Gly	Ile	Gln	Glu	Leu	Ala	Glu	Gln	Leu	Gln		
		50				55					60						
aag	att	atg	gaa	gag	tct	gga	gct	gtg	gct	act	gca	acc	agt	gtc	cct		241
Lys	Ile	Met	Glu	Glu	Ser	Gly	Ala	Val	Ala	Thr	Ala	Thr	Ser	Val	Pro		
	65				70				75						80		
gct	cag	ggc	aca	gcc	aga	aca	gaa	cat	ttt	gtg	gac	caa	cac	agg	caa		289
Ala	Gln	Gly	Thr	Ala	Arg	Thr	Glu	His	Phe	Val	Asp	Gln	His	Arg	Gln		
			85					90						95			

gca ctc att gcc agg gtc aca gaa gtt gat ggt ttg ctg gat gct ctg 337
Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Leu Leu Asp Ala Leu
100 105 110

tat ggc aat gtg ctg act gaa gga cag tac cag gca gtt cgt gca gag 385
Tyr Gly Asn Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala Glu
115 120 125

acc acc aac caa aac aag atg agg aag ctc ttt agc ttt gct cca gcc 433
Thr Thr Asn Gln Asn Lys Met Arg Lys Leu Phe Ser Phe Ala Pro Ala
130 135 140

tgg aac ctg acc tgc aag aac ttg ttc ctt gag gcc ttg agg caa aca 481
Trp Asn Leu Thr Cys Lys Asn Leu Phe Leu Glu Ala Leu Arg Gln Thr
145 150 155 160

cag ccc tac ttg gtg aca gac ctg gaa cag agc tga g gtatcttttc 528
Gln Pro Tyr Leu Val Thr Asp Leu Glu Gln Ser *
165 170

cagctacaca tctagctcct gggtttgtat acaaaaatttt ctaaaaacaa gtttgtattt 588
gtgttttctc gaaaaaa 605

<210> 23
<211> 171
<212> PRT
<213> Rattus Norvegicus

<400> 23
Phe Lys Ile Lys Leu Leu Thr Ala Pro Val Arg Glu Gly Tyr Gly Arg
1 5 10 15
Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Pro Ile Asp Leu Thr Asp
20 25 30
Lys Leu Val Xaa Tyr Tyr Leu Glu Gly Tyr Gly Leu Glu Leu Thr Met
35 40 45
Thr Val Leu Arg Asp Met Gly Ile Gln Glu Leu Ala Glu Gln Leu Gln
50 55 60
Lys Ile Met Glu Glu Ser Gly Ala Val Ala Thr Ala Thr Ser Val Pro
65 70 75 80
Ala Gln Gly Thr Ala Arg Thr Glu His Phe Val Asp Gln His Arg Gln
85 90 95
Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Leu Leu Asp Ala Leu
100 105 110
Tyr Gly Asn Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala Glu
115 120 125
Thr Thr Asn Gln Asn Lys Met Arg Lys Leu Phe Ser Phe Ala Pro Ala
130 135 140
Trp Asn Leu Thr Cys Lys Asn Leu Phe Leu Glu Ala Leu Arg Gln Thr
145 150 155 160
Gln Pro Tyr Leu Val Thr Asp Leu Glu Gln Ser
165 170

<210> 24
<211> 713
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS

<222> (75)...(605)

<400> 24

```

ccacgcgtcc gacttcctcc tggtcggcgg ctgcagcggg gtgagcggcg gcagcggccg      60
gggatcctgg agcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg      110
          Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu
              1              5              10

gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg      158
Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu
          15              20              25

tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg      206
Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
          30              35              40

ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac      254
Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
          45              50              55              60

ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg      302
Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met
          65              70              75

ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc      350
Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly
          80              85              90

ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg agg gtc aca      398
Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr
          95              100              105

aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc ctg acg gat      446
Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp
          110              115              120

gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca agc aag atg      494
Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met
          125              130              135              140

cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc tgc aag gac      542
Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp
          145              150              155

ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg gtg gag gac      590
Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp
          160              165              170

ctg gag cgg agc tga ggctccttcc cagcaacact ccggtcagcc cctggcaatc      645
Leu Glu Arg Ser *
          175

ccaccaaadc atcctgaadc tgatcttttt atacacaata tacgaaaagc cagcttgaaa      705
aaaaaaaaa
          713

```

<210> 25

<211> 176

<212> PRT

<213> Homo Sapiens

<400> 25
 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
 1 5 10 15
 Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu
 20 25 30
 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
 35 40 45
 Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
 50 55 60
 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
 65 70 75 80
 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Leu His Phe Ile
 85 90 95
 Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn Val Glu Trp
 100 105 110
 Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu Gln Tyr Gln
 115 120 125
 Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg Lys Leu Phe
 130 135 140
 Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu Leu Leu Gln
 145 150 155 160
 Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu Glu Arg Ser
 165 170 175

<210> 26
 <211> 414
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> (75)...(404)

<400> 26
 ccacgcgtcc gacttcctcc tggctcggcgg ctgcagcggg gtgagcggcg gcagcggccg 60
 gggatcctgg agcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg 110
 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu
 1 5 10
 gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg 158
 Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu
 15 20 25
 tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg 206
 Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
 30 35 40
 ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac 254
 Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
 45 50 55 60
 ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg 302
 Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met
 65 70 75
 ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc 350
 Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly
 80 85 90
 tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca gcc 398

Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala
95 100 105

aag cca g
Lys Pro
110

405

<210> 27
<211> 110
<212> PRT
<213> Homo Sapiens

<400> 27
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
1 5 10 15
Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu
20 25 30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
35 40 45
Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
50 55 60
Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
65 70 75 80
Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala
85 90 95
Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro
100 105 110